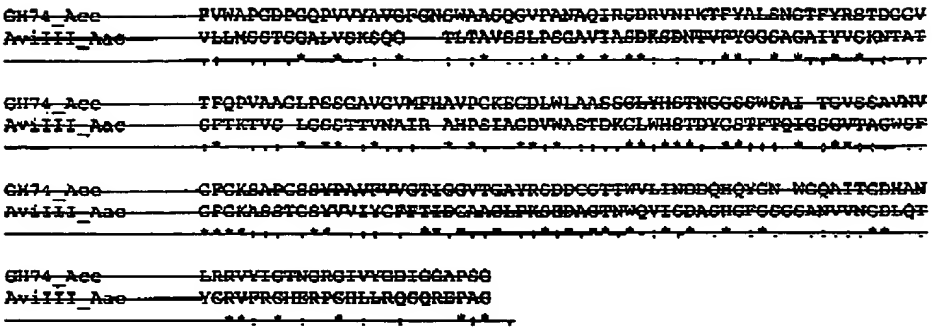
Amendments to the claims:

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified AvilII peptide with cellulase activity and ~~, said AvilII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme~~ having at least ~~70~~ 90% identity to SEQ ID NO. 1, said AvilII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74 Ace) enzyme and a carbohydrate binding domain (CBD) III. ~~, the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvilII_Aac):~~

```
GH74_Ace      ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac    AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
              *.:*.***.**. ****.*.*****.*.*.*.******.**.:.:  *.**.****

GH74_Ace      WNNWGYNGVVGIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AviIII_Aac    NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTSTKLPFKVG
              .:.*  *. :.*.**.:.*.:*.:*.*******.****.*.****.***.**  *.****.*

GH74_Ace      GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII_Aac    GNMPGRGMGERLAVDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSFTWTGTYFQDSSS
              *****************..:******.**.***.***.*****::*.*.*  .**:  :..:

GH74_Ace      TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T
AviIII_Aac    T--YTSDPVGIAWVTFDETSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
              *. *.**. *:.**:**:.*.*.*.*..:.:*******..:.**.*.*.****  *.*.*

GH74_Ace      GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF
AviIII_Aac    GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP----TSLASTYY
              **:******:.*.:.:***:.*:.******:.*.*.*.:.:**.**:***   *.*.*.*:

GH74_Ace      GYSGLTIDRQHPNTIMVATQIGWWPDTIIFRSTDGGATWTRIWDWTGYPNRSLRYVLDIG
AviIII_Aac    GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYYSYDIG
              **.**.:*.*.*.*.****.  .****.:******.*****.**.*.**.:.  . *  ***

GH74_Ace      AEPNLTFGVQPNPFVTSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII_Aac    -NAPWIQDTTSTDQFP--VRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
                 **.     ....      :.***.**.*******.*.:.*****.*.*.*.:***.***  :.

GH74_Ace      HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTGV
AviIII_Aac    TVKGLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFWHSDLDAAPNQAHTPTYGTTNGI
              .....*.**.**..**.**.*..*.**.**.***.*.*..*.*.*.....*.:.*..*...

GH74_Ace      DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac    DYAGNKPSNIVRSGASDDYP------TLALGSNFGSTWPADYAAGTGTGTGAVALSADGDT
              .**..**.***.*.*.... ..      .*.*.*..*.*.*.*. .....*..*.**.****.
```



2. (Previously Presented) The composition of claim 1 wherein the AviIII peptide is further defined as comprising a linker and a signal sequence.

3. (Cancelled)

4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 90 amino acids.

6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.

7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Previously Presented) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Previously Presented) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Presented) An isolated AviIII peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the AviIII polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[.]

16-27 (Cancelled)

28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

a) a polypeptide sequence of SEQ ID NO: 3;
b) a polypeptide sequence of SEQ ID NO: 4;
c) a polypeptide sequence of SEQ ID NO: 5;
d) a polypeptide sequence of SEQ ID NO: 1; and
e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Presented) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemaglutinin, glutathione S-tranferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII_Aac):

```
GH74_Ace        ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac      AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDNVG
                *::*.***.**. **** *. ***** .* *: *.****** ** :: :  * **:****

GH74_Ace        WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AviIII_Aac      NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG
                 :.*   *: ::*:**::*::*:.*******.**** *:****:*** **  * ****:*

GH74_Ace        GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII_Aac      GNMPGRGMGERLAVDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSFTWTGTYPQDSSS
                ******************::.****** **:***:*** *****::*.*...***: :.:.

GH74_Ace        TTGYQSDIQGVVWVAPDKSSSSLGQASKTIPVGVADPNNPVFWSRDGGATWQAVPGAP-T
AviIII_Aac      T--YTSDPVGIAWVTPDSTSGSSGSATPRIPVGVADAGKSVPKSEDAGATWAWVSGEPQY
                *  * **  *:.**:**.:*.* *.*:  *******..:.** *.*.****  *.* *

GH74_Ace        GPIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYP
AviIII_Aac      GPLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY
                **:*****:.* ::.***: :* .*****:.* * *:.:***.** ***   *. *. *:
```

```
GH74_Ace        GYSGLTIDRQHPNTIMVATQISWWPDTIIPRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac      GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWENNGYPSINYYYSYDIS
                **.**::* * *.*:***:  .**** :******.****: **:*..**. .  *  ***

GH74_Ace        AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII_Aac      NAPWIQDTTSTDQFP--VRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
                  **:   ...:       ::*** **:*****:*:: ***** *:*. :***:***  ::

GH74_Ace        HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV
AviIII_Aac      TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI
                 : .:. *:** ** .**:**.*..*:**:** *** *:*: *.*.  : :*.: *. ..:

GH74_Ace        DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac      DYAGNKPSNIVRSGASDDYP-----TLALSSNPGSTWYADYAASTSTGTGAVALSADGDT
                *** :** ***:*: *  .       :*:*:: *..*: .  ..  *  *:** ****.

GH74_Ace        FVWAPGDPGQPVVYAVGPGNSWAASQGVPAMAQIRSDKVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac      VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT
                .:  .. .*  *  : *   : :* ..:*:.* * **: : ..**. * *::* *.: ..

GH74_Ace        TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac      SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
                :*  ..: * ** :*..:  * *.  **:* ::..**:***: **::: * :**::. ..

GH74_Ace        GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac      GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT
                ****::. .** .:: . **.*.:* ::*:*.**.* :*.* .* :*.  .:.:.**  .

GH74_Ace        LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac      YGRVFRGHERPGHLLRQSQREPAG
                  **: * :  * :  :    *:* .
```

48. (New) The composition of claim 47 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (New) A composition comprising a substantially purified AviIII peptide having at least 99% identity to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (New) The composition of claim 49 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII_Aac):

```
GH74_Ace        ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac      AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
                *::*.***.**. **** *. ***** .* *: *.****** ** :: :  * **:****

GH74_Ace        WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AviIII_Aac      NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG
                 :.*   *: ::*:**::*::*:.******.**** *:****:*** **  * ****:*

GH74_Ace        GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLMRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII_Aac      GNMPGRGMGERLAVDPNKNSILYFGARSGHGLMKSTDYGATWSNVTSFTWTGTYPQDSSS
                ******************:::.****** **:***:*** ******::*.*. .***: :.:.
```

```
GH74_Ace        TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVPWSRDGGATWQAVPGAP-T
AviIII_Aac      T--YTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
                *  * **  *:.**:**.:*.* *.*: ******* ..:.** *.*.**** *.* *

GH74_Ace        GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKPSVTSGTWTRISPVPSTDTANDYF
AviIII_Aac      GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY
                **:*****:.* ::.***: :* .*****:.* * *:.:***.** ***   *. *. *:

GH74_Ace        GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac      GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYYSYDIS
                **.**::* * *.*:***:  .**** :****** ****: **:*..**. .  *  ***

GH74_Ace        AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII_Aac      NAPWIQDTTSTDQFP--VRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
                  **:   ...:       ::*** **:*****:*:: ***** *.*. :***:***  ::

GH74_Ace        HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV
AviIII_Aac      TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI
                 : .:. *:** ** .**:**.*..*:**:** *** *:*: *.*.  : :*.: * ..:

GH74_Ace        DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac      DYAGNKPSNIVRSGASDDYP-----TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT
                *** :** ***:*: *  .       :*:*:: *..*: .  ..  *  *:** ****.

GH74_Ace        FVWAPGDPGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTPYRSTDGGV
AviIII_Aac      VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT
                .:  .. .*  *  : *   : :* ..:*:.* * **: : ..**. * *::* *.: ..

GH74_Ace        TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac      SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
                :*  ..: * ** :*..:  * *.  **:* ::..**:***: **::: * :**::. ..

GH74_Ace        GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac      GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT
                ****::. .** .:: . **.*.:* ::*:*.**.* :*.* .* :*.  .:.:.**  .

GH74_Ace        LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac      YGRVFRGHERPGHLLRQSQREPAG
                  **: * :  * :  :    *:* .
```

51. (New) The composition of claim 50 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified AviIII peptide having an amino acid sequence identical to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain GH74_Ace has a sequence identical to SEQ ID NO. 3.